

0280

#2

OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/015,536

DATE: 01/10/2002  
 TIME: 14:48:56

Input Set : A:\103-00.app  
 Output Set: N:\CRF3\01102002\J015536.raw

ENTERED

3 <110> APPLICANT: Kranz, David M.  
 4 Starwalt, Scott  
 5 Bluestone, Jeffrey A.  
 7 <120> TITLE OF INVENTION: Mutated Class II Major Histocompatibility Proteins  
 9 <130> FILE REFERENCE: 103-00  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/015,536  
 12 <141> CURRENT FILING DATE: 2001-12-10  
 14 <150> PRIOR APPLICATION NUMBER: 60/254,248  
 15 <151> PRIOR FILING DATE: 2000-12-08  
 17 <160> NUMBER OF SEQ ID NOS: 28  
 19 <170> SOFTWARE: PatentIn Ver. 2.0  
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221 aacgggacgc agcgcatacg gctcgtgacc agatacatct acaaccggga ggagtacctg 180
222 cgcttcgaca gcgacgtggg cgagtaccgc gcggtgaccg agctggggcg gcactcagcc 240
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224 cacaactacg aggagacgga ggtccccacc tccctgcggc ggcttgaaca gcccaatgtc 360
225 gccatctccc tgtccaggac agaggccctc aaccaccaca aacctctggg ctgttcgggtg 420
226 acagatttct acccagccaa gatcaaagtg cgctggttca ggaatggcca ggaggagaag 480
227 tgggggtctc atccacacag cttattagga atggggactg gaccttccag gtctctgtca 540
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230 acgacattga ggccgaccac gtaggcttct atgtacaact gtttatcagt ctcttgagga 720
231 cattggccag tacacacatg aatttgatgg tgatgagttg ttctatgttg acttgataa 780
232 gaagaaaact gtctggaggc ttcctgagtt tggccaattg atactctttg agccccaagg 840
233 tggactgcaa aacatagctg cagaaaaaca caacttggga atcttgacta agaggtcaaa 900
234 ttccacccca gctaccaatg aggctcctca agcgactgtg ttccccaagt cccctgtgct 960
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236 catcacatgg ctcagaaata gcaagtcagt cacagacggc gtttatgaga ccagcttctt 1080
237 cgtcaaccgt gaccattcct tccacaagct gtcttatctc accttcatcc cttctgatga 1140
238 tgacatttat gactgcaagg tggagcactg ggcctggag gagccgggtc tgaacaactg 1200
239 ggaacaaaag cttatttctg aagaagactt gtgataaaga tct                                     1243
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242 <211> LENGTH: 411
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248     peptide
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251 Ala Ser Gly Gly Leu Lys Gly Gly Gly Ser Leu Val Pro Arg Gly
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254 Ser Gly Gly Gly Gly Ser Gly Asp Ser Glu Arg His Phe Val His Gln
255   20           25           30

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257 Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu
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260 Val Thr Arg Tyr Ile Tyr Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser
261          50          55          60
263 Asp Val Gly Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg His Ser Ala
264 65          70          75          80
266 Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp
267          85          90          95
269 Thr Ala Cys Arg His Asn Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu
270          100          105          110
272 Arg Arg Leu Glu Gln Pro Asn Val Ala Ile Ser Leu Ser Arg Thr Glu
273          115          120          125
275 Ala Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr
276          130          135          140
278 Pro Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr
279 145          150          155          160
281 Val Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe
282          165          170          175
284 Gln Val Leu Val Met Leu Glu Met Thr Pro His Gln Gly Glu Val Tyr
285          180          185          190
287 Thr Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu
288          195          200          205
290 Trp Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Glu Asp Asp Ile Glu
291 210          215          220
293 Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly
294 225          230          235          240
296 Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr
297          245          250          255
299 Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly
300          260          265          270
302 Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala
303          275          280          285
305 Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro
306          290          295          300
308 Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val
309 305          310          315          320
311 Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe
312          325          330          335
314 Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr
315          340          345          350
317 Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe
318          355          360          365
320 His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr
321          370          375          380
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324 385          390          395          400
326 Trp Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
327          405          410
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VERIFICATION SUMMARY

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Input Set : A:\103-00.app

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12